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Result
No.
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Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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108
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693.5
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungl:*

4: sp_human:*
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Match
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228.6
221.3
221.3
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Gapop 10.0 ,
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:*
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(c) 1993 - 2000
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_		O68497 clostridium	Q9kp90 vibrio chol	Q9jyiO neisseria m	P94783 citrobacter	Q38795 amaranthus	Q41716 xanthium sp		Q41769 zea mays (m	. Q42768 gossypium h	Q59272 caulobacter	Q42767 gossypium h	bassia sc	Q41768 zea mays (m		O49229 chlamydomon	Q45396 corynebacte	049210 volvox cart				Q05767 brassica na	022578 volvox cart	_	Q9pcg0 xylella fas

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01-MAY-1999 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
PYRUVATE DEHYDROGENASE.
SCIA9.19.
PFAM; PF00205; TPP_enzymes; 1.
Pyruvate.
SEQUENCE 580 AA; 62503 MW;
                                                                                                 Kinashi H., Kieser H.M., Denapaite D., Eichner A
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; ALO34446; CAA22389.1; -.
INTERPRO: IPR000399; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
Bentley S.D., Parkhill J., I
Submitted (DEC-1998) to the
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Saunders D.C.,
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MEDLINE=97000351; PubMed=8843436;
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EMBL/GenBank/DDBJ databases.
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Last sequence up
Last annotation
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Query Match
Best Local Similarity
Matches 331; Conserv

Conservative

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Score 1713; DB 2; Pred. No. 5.6e-109; 2; Mismatches 149;

Length 580; Indels

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01-OCT-2000
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Beloin C., Ayora S., Extey N., ...

Rasahara Y., Alonso J.C., Le Hegarat F.;

Rasahara Y., Al
STRAIN-168;

MEDLINE-98044033; PubMed-9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Choi S.K., Codani J.J., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
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Nature 390:249-256(1997).
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B.J., Haga K., Haiech J., Harwood C.R., H
ppel S., Hosono S., Hullo M.F., Itaya M.,
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                                                                                                                                                                                                                                                                                                                                                                                                 SGYCEMVNGGEQGERILHHAIQSTMAGKGVSVVVIPGDIAKEDAGDGTYSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKEC
                                                                   VLPDDLPYVTGPIGLLGSKASDNMIQGCDTLLMVGSSFPYSEWLPEEGQARGVEIDIDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEVGCCVATSGPGAVHLLNGLYDAKLDHQPVVAVVGQQKRLSLGTHYQQETALDQLFADV
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HIGRRTTVKYPVTGDVAATIENILPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNVEK
                                                                                                            YIQHENPPEVGMSGLLGYGACVDASNEADLLILLGTDFPYSDFLPKDNVA---QVDINGA
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                                                                                                                                                                                                             WSRPRVLPDLDELRKAADVLNAGNKVAMLVGQGAANAEAEVKEVAELLGAGVAKALLGRQ
                                                                                                                                                                                                                                                                                 SGTPVVFPDPTEAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQ
                                                                                                                                                                                                                                                                                                                                                            SEYCQMVVHPGQARHVVDRAFKTALTTRGVATIIIPNDIQEEEAQPSPPREHGSVFSSVG
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) to the EMBL/GenBank/DDBJ
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 693.5; DB 2;
Pred. No. 3.1e-39;
)8; Mismatches 252;
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                                                                                                                                                      Query Match
Best Local Similarity
Matches 164; Conserv
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INTERPRO; IPR001052; -.
INTERPRO; IPR003252; -.
PFAM; PF00205; TPP_enzymes; 2
PFAM; PF00301; rubredoxin; 1.
PRODOM; PD001610; -; 1.
                                                                                                                                                                                                                                                                                                                                                           Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLEEL. 05, Created)
01-JAN-1998 (TREMBLEEL. 05, Last sequence update)
01-CCT-2000 (TREMBLEEL. 15, Last annotation updat
PYROUVATE DEHYDROGENASE / ACETOLACTATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum
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                                                                                                                                                                                                                                                                                                                                       HSSP;
                  125
                                         115 QPAVCMAVAGPRASNLITGLLDAALDRAPVLAVTGHVETYRIGTGASQEIDQHSLFESFS
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GYCEMVNGGEQGERILHHAIQSTMAGKGVSVVVIPGDIAKEDAGDGTYSNSTISSGTPV-
                                                         GRPVVLEFKVDAEIAPIPPHIMKEQGKKAIKAA
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P00269; 1RB9.
                                                                                                                                                                                                                          553 AA;
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                                                                                                                                                                                                                                                            1. 2.
                                                                                                                                                      95;
                                                                                                                                                  Score 637; DB 1
Pred. No. 2e-35;
5; Mismatches 2
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Query Match
Best Local :
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01-NOV-1999
01-OCT-2000
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PROSITE; PS00187; TPP_ENZYMES; 1.
Lyase; Flavoprotein; Thiamine pyrophosphate.
SEQUENCE 587 AA; 63837 MW; A31D9424A71FE440
                                                                                                                                                                                                                                                                                                                                                                                           "Development o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TYEMBLEEL 12, Created)
01-NOV-1999 (TYEMBLEEL 12, Last sequence update)
01-CCT-2000 (TYEMBLEEL 15, Last annotation update)
ACETOHYDROXYACID SYNTHASE LARGE SUBUNIT (EC 4.1.3.18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0F8160
                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                          Gardner W.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus maripaludis
                                                                                                                                                                                                                                                                                                                    INTERPRO;
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124
                            126
                                                                                                                                                                                                                                                                                                                                  !- SIMILARITY: WITH OTHER ENZYMES MBL; AF118061; AAD28737.1; -. SSP; P06169; 1PVD.
                                                          64
                                                                                                                                                                                               Local Similarity
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                                                        LVEGQPEFGTDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYPGPVLIDIVTDP
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                                                                                                                    {\tt AEAMMKALEAENVKVLFGYPGGQLLPFYDALYQSDFLHILTRHEQAAAHAADGYARASGD}
HNFQIQKTSEIPKIFRKAFEIAKTGRPGAVHVDLPKDVQDDDLDLEKYPIPAEINLQGYK
                          YCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTY---
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            of integrative
                                                                                                                                                                                                                                                                                                                                                                                                                         Whitman W.B.;
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Pred. No. 5.5e-34;
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                                                                                                                                                                                  Indels
                                                                                                                                                                                                             Length
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                                                                                                               HSSE; POC169; LFVL.
HSSE; POC169; LFVL.
INTERPRO, IPRO00399; -
PFAM; PF00205; TPP_enzymes; 1.
PROSITE; PS00187; TPP_ENZYMES; 1.
PROSITE; PS00187; TPP_ENZYMES; 1.
PROSITE; PS00187; AB; 62674 MW; A9;
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01-JAN-1998
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                                                                                                                                                                                                                                                                                     -!- SIMILARITY: WITH OTHER ENZYMES EMBL; AE000905; AAB85919.1; -. HSSP; P06169; 1PVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; 
Methanobacterium.
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                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                              DNA RCS. 3:109-136(1996).
EMBL; D90910; BAA17977.1;
HSSP; P06169; 1PVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain Bacteria; Cyanobacteria; 
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                                                                                                                                                                    PF00205; TPP
NCE 621 AA;
      164;
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Ima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Thi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                  Similarity
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(TremBLrel. 02, Last sequent (TremBLrel. 15, Last annumated)
Y ACID SYNTHASE.
      Conservative
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                                                                                                                                                                    TPP_enzymes; 1. AA; 67730 MW;
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%; Score 567; DF
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113; Mismatches
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annotation
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KSVRITDPKKVREQLAEALAYPGPVLIDIVT--DPNAL-SIPPTITWEQVMGFSKAATR
                                                                   HQLPLKAVVFNNSSLGMVK------LEMLVEGQPEFGTDHEEVNFAEIAAAAGI
                                                                                          FLNN--GPRRWISSAGLGTMGFGLPAAMGAKVGVGDEAVICISGDASFQMNLQELGTLAQ
                                                                                                      PKDNVAQVDINGAHIGRRTTVKYPVTGDVAATIENILPHVKE------KTDRSFLDRML
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                                                                                                                                                                                                                                                                             ---- VNLPGYRPTYKGNPRQINAALQLLEQARNPLLYVGGGAIAANAHAQVQEFAERFQL
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                                                                                                                                                                                    SRAKVIHIDIDPAEVGKNRAPDVPIVGDVRHVLEQLLQRARELDYPTHPHTTQAWLNR--
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O08353; PRELIMINARY;
O1.JUL-1997 (TrEMBLrel. 04,
O1.JUL-1997 (TrEMBLrel. 04,
O1.MAY-2000 (TrEMBLREL. 13,
ACETOHYDROXYACID SYNTHASE L.
(ACETOLACTATE SYNTHASE)
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=97254452; PubMed=9099862;
Bowen T.L., Union J., Tumbula D.L.,
Bowen T.L., Union J., Tumbula D.L.,
"Cloning and phylogenetic analysis (
"Cloning and phylogenetic analysis (
                                                                                                                                                                                                                                                                       PROSITE; PS00187; TPI
Lyase; Flavoprotein;
SEQUENCE 599 AA;
                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanococcus. NCBI_TaxID=42879;
                                                                                                                                                                                                       -!- SIMILARITY: WITH OTHER EMBL; U35458; AAB53488.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus aeolicus.
                                                                                                                                                                                   NTERPRO;
MILARII.

U35458; AABbor.

RPRO; TPR000399; -.

R; PF00205; TPP_enzymes; 1.

"TTE; PS00187; TPP_ENZYMES; 1.

"voprotein; Thiamine pvoprotein; 65423 MW;
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(. 04, Last sequence update)
1. 13, Last annotation update
HASE LARGE SUBUNIT (EC 4.1.3.
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                                               pyrophosphate.
59630C57DECE0D62
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on Methanococcus aeolicus.
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: 4.1.3.18)
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Query Match
Best Local Similarity

18.4%; 27.3%;

Score Pred.

549; DB 8; No. 2.2e-29;

Length

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Best Local
Matches 16
                                                                                                                                                                                                                                                            Cyanidium caldarium (Gal
Chloroplast.
Eukaryota; Rhodophyta; E
Cyanidium.
EMBL; AF022186; AAB82660.1; -.
HSSP; P06.69; 1PVD.
MENDEL; 23.174. Cyaca;1145;23174.
INTERPRQ; IPR000399; -.
PFAN; P000205; TPP_enzymes; 1.
PROSITE; P800187; TPP_ENZYMES; 1.
Chloroplast; Flavoprolein; Lyase; Thiamine pyrophosphate.
SEQUENCE 585 AA; 65123 MW; 17D95558C6F76011 CRC64;
                                                                                                                                                                                                                                                                                                                                                                O19929;
O1-JAN-1998
O1-JAN-1998
O1-OCT-2000
                                                                                                                                         Gloeckner G., Rosenthal A., Valentin K.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: WITH OTHER ENZYMES WHICH REQU
                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 0: 01-OCT-2000 (TrEMBLrel. 1: ACETOHYDROXYACID SYNTHASE
                                                                                                                                                                                               STRAIN-RK1;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=2771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVFNNSSLGMV-KLEMLVEGQPE----FGTDHEEVNFAEIAAAAGIKSVRITDPKKVREQ
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                                                                                                                                                                                                                                                                                                              (Galdieria sulphuraria).
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15,
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5, Last
LARGE S
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Pred. No. 1.5e-30;
9; Mismatches 255
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Q59950;
Q1-NOV-1996
Q1-NOV-1996
Q1-CCT-2000
EMBL; M75
HSSP; P06
INTERPRO;
           "Molecular characterization of the genes synthase in the cyanobacterium Spirulina J. Gen. Microbiol. 138:1399-1408 (1992) - i- CATALYTIC ACTIVITY: 2-ACETOLACTATE + i- COPACTOR: THIAMIN PYROPHOSPHATE. EMBL; M75906; AAA26594.1; - HSSP; P06169; 1PVD.
                                                                                                    Milano A.,
Riccardi G
                                                                                                                          SEQUENCE FROM N.A. MEDLINE=92381487;
                                                                                                                                                               NCBI_TaxID=1156;
                                                                                                                                                                            Spirulina platensis.
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                          KDLKSKIERIISTPGPLLIDCIVATSENCYPMIAPGKSNSQMLGLTK
                                                                                                                                                                                                                                                                                                                                                                               KKVREQLAEALAYPGPVLID--IVTDPNAL-SIPPTITWEQVMGFSK
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  IPR000276;
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                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                           PubMed=1512571;
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Last annotation update)
(EC 4.1.3.18) (ACETOLACTATE
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Matches
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SEQUENCE
                                                                                 Aquifex aeolicus.
Bacteria; Aquificales;
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                     SEQUENCE FROM N.A
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                                                            NCBI_TaxID=63363;
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O1-CCT-2000 (TrEMBLrel. 15, Created)

O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-CCT-2000 (TrEMBLrel. 15, Last annotation update)

O1-CCT-2000 (TrEMBLrel. 15, Last annotation update)

O1-CCT-2000 (TrEMBLREL. 15, Last annotation update)

O1-CCT-2000 (TrEMBLREL. 15, Last sequence update)

O1-CCT-2000 (TrEMBLREL. 15, Created)

O1-CCT-2000 (TrEMBLREL. 15, Last sequence update)

O1-CCT-2000 (TrEMBLREL. 15, Last sequence update)

O1-CCT-2000 (TrEMBLREL. 15, Last sequence update)

O1-CCT-2000 (TrEMBLREL. 15, Last sequence update)
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Deckert G., Warren P.V., Gaasterl
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Best Loc
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O28554;
O1-JAN-1998
O1-JAN-1998
O1-OCT-2000
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submitted (PEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AQ233324; AAF33483.1; -.
SEQUENCE 548 AA; 59224 MW; 6587AAE9E6E2BE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU;
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ILVG_1.
                                                       028554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteri Salmonella.
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                                                                                                                                                                                                                                                    FRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSS
                                                                                                                                                                                                                                                                                                                       HNVEKHVPIHPEYVASILNELADK----DAVFTVDTGMCNVWHARYI--ENPEGTRDFVGS
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                                                                                                                           GPYLLHVSID
                                                                                                                                                     GPVLIDIVTD
                                                                                                                                                                               {\tt LGMVRQWQQLFFQERYSETTLTDNPD--FLMLASAFGIPGQHITRKDQVEAALDTMLASE}
                                                                                                                                                                                                   LGMVKLEMLVEGQPEFG----TDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYP
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                                                                                                                                                                                                                                                                                                                                                 AEMNKLRQAHVALQGD----LNSLLPALQQPLKIDAWRQSCAELRAEHAWR-----YD
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(TrEMBLrel.) (TrEMBLrel.)
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                                                       PRELIMINARY;
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Mismatches
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databases.
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Best Local S
Matches 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; AF1
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM, PF00205; TPP_enzymes; 1.
PROSITE; PS00187; TPP_ENZYMES; 1.
Hypothetical protein; Flavoprotein; Lyase; Thiamine pyrophosphate.
SEQUENCE 552 AA; 59974 MW; 69A4132C525F8245 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, reducing archaeon Archaeoglobus fulgidus.";
Nature 390.364-370(1997).
-!- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP. EMBL, AE000985, AAB89531.1;
TIGR; AF1720; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRALN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F.
Ketching K n. Po-2-----
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                 GMVKLEMLVEGQPEFGTDH--
                                            GLGTMGFGFPAAMGAQVAFPEKTVIDIAGDGSFFMNIQELATCVKYEIPVKVLVLNNGYL
                                                            RHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSL
                                                                                                                                                                                GAHIGRRTTVKYPVTGDVAATIENILPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNV
                                                                                                                                                                                                             ETHPLSLGFAGMHGTKYANYALSESDLIIAVGCRF--
                                                                                                                                                                                                                                                                                           VFPDPTEAAALVEAINNAKSYTLFCGAGV--KNARAQVLELAEKIKSPIGHALGGKQYIQ 241
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                                                                                               KKRYPLKYKKEGFKPQYVIERACEIM-PDAIITTEVGQNQMWAAQFFKT-KYPRQFITSG
                                                                                                                                                      PAEIGKNVRVDVPIVGDA---
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  EEVNFAEIAAAAGIKSVRITDPKKVREQLAEAL
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DB 1; .9e-27;

Length

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Zhou В.,

L.,

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SDRTTGNVAMFAPEAKIIHIDID

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01-MAY-1999 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
ACETOLACTATE SYNTHASE.
SCBD9.24.
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PROSITE;
SEQUENCE
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Bentley S.D., Parkhill J., B
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Bacteria; Firmicutes; Actinobacteria; Actinobacterid Actinomycetales; Streptomycineae; Streptomycetaceae;
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INTERPRO: IPRO00399; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436; Redenbach M., Kleser H.M., Denapaite Kinashi H., Hopwood D.A.;
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TE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.

TE; PS00187; TPP_ENZYMES; UNKNOWN_1.

ENCE 613 AA; 65223 MW; 8F1378EB37003429 CRC64;
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  HTGRRTTVKYPVTGDVAATIENTLPHVKEKTDRSFLDRMLKAHERKLSSVVETYT--HNV
                                          DSHPLHVGMPGMHGAVTAVTALQKADLIVALGARFDDRVTGKLDSFAPHAKIVHADIDPA
                                                                                                                                  TKPHAKQIREAAKLISAAKRPVLYVGGGVLKAKATAELKVLAELTGAPVTTTLMALGAEP
                                                                                                                                                                                 VFPDPTEAAALVEAINNAKSVTLFCGAGVKNAR--AQVLELAEKIKSPIGHALGGKQYIQ
                                                                                                                                                                                                                              KHSFLVTKAEDIPRVIAQAFHIASTGRPGPVLVDIPKDILQKKTTFSWPPVMDLPGYRPV
                                                                                                                                                                                                                                                                         GYCEMVNGGEQGERILHHATQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPV
                                                                                                                                                                                                                                                                                                                      KVGVCMATSGPGATNLVTPIADANLDSVPLVAITGQVVSSAIGTDAFQEADIVGITMPIT
                                                                                                                                                                                                                                                                                                                                                              ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECS
                                                                                                                                                                                                                                                                                                                                                                                                              AQSLIRSLEEVGADTVFGIPGGTILPAYDPLMDSTRVRHVLVRHEQGAGHAATGYAQATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQSD-IEWVHVRNEEAAAFAAGAESLITG
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(FEB-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000847; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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N. A.
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score :
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No. 1.
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Streptomyces
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.5e-26;
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hromosome.";
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Matches 164
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MEDILIN-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.

McDonald L., Utterback T.R., Malek J.A., Phillips C.A., Richardson Heidelberg J., Sutton M.D., Pratt M.S., Phillips C.A., Richardson Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.,

"Evidence for lateral gene transfer between Archaea and Bacteria genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999),
                                                                                                                                                                                                              PFAM; PF00205; TPP_enzymes; 1.

PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.

PROSITE; PS00187; TPP_ENZYMES; 1.

Flavoprotein; Lyase; Thiamine pyrophosphate.

SEQUENCE 584 AA; 64431 MW; B2F69C3D6A4F1205 CRC64;
                                                                                                                                                                                                                                                                                                       HSSP; P06169; 1PVD.
TIGR; TM0548; -.
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TM0548.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                             AEQLIDTLEAQGYKRIYGLYGDSLNPIYDAY--RQSDIEWYHYRNEEAAAFAAGAESLIT 63
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                                               SGYCEMVNGGEQGERILHHAIQ----STMAGKGVSVVVIPGDIAKEDAGDGTYSNST-I
                                                                        GELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKEC
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                                                                                                                                                     164;
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermotogales;
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(TrEMBLrel. 12, Last sequence up
(TrEMBLrel. 15, Last annotation
E SYNTHASE, LARGE SUBUNIT.
                                                                                                                                                     Conservative
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-LPYAIKEMFYVATTGRPGPVLLDFPKDTQTAE-GEFNYPDTVEI
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Pred.
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                                                                                                                                                   Mismatches
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No. 3.4
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3.4e-26;
3s 232;
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Search completed: March 17, 2001, 21:55:06 Job time: 2537 sec